

Fig. 1

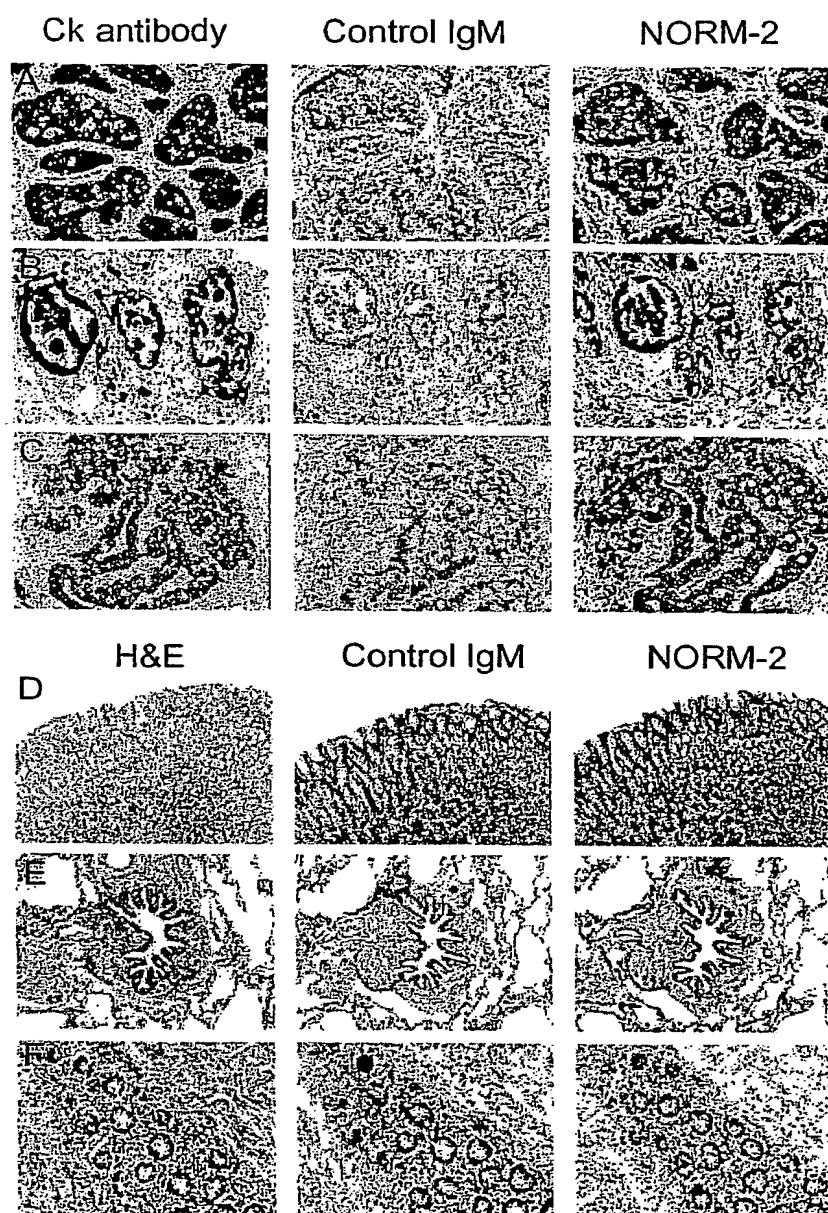


Fig. 2

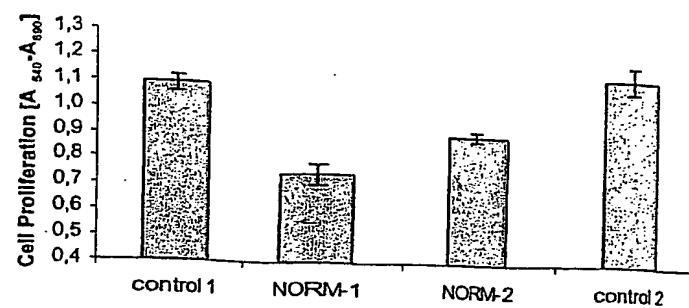


Fig. 3

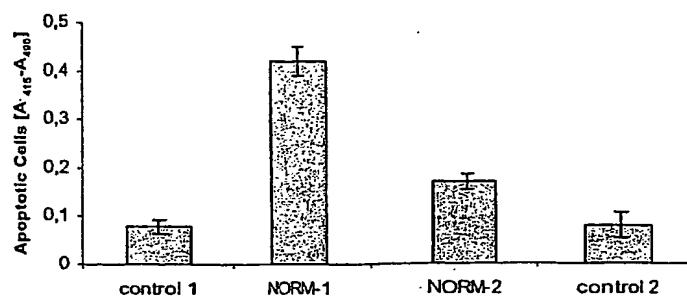


Fig. 4

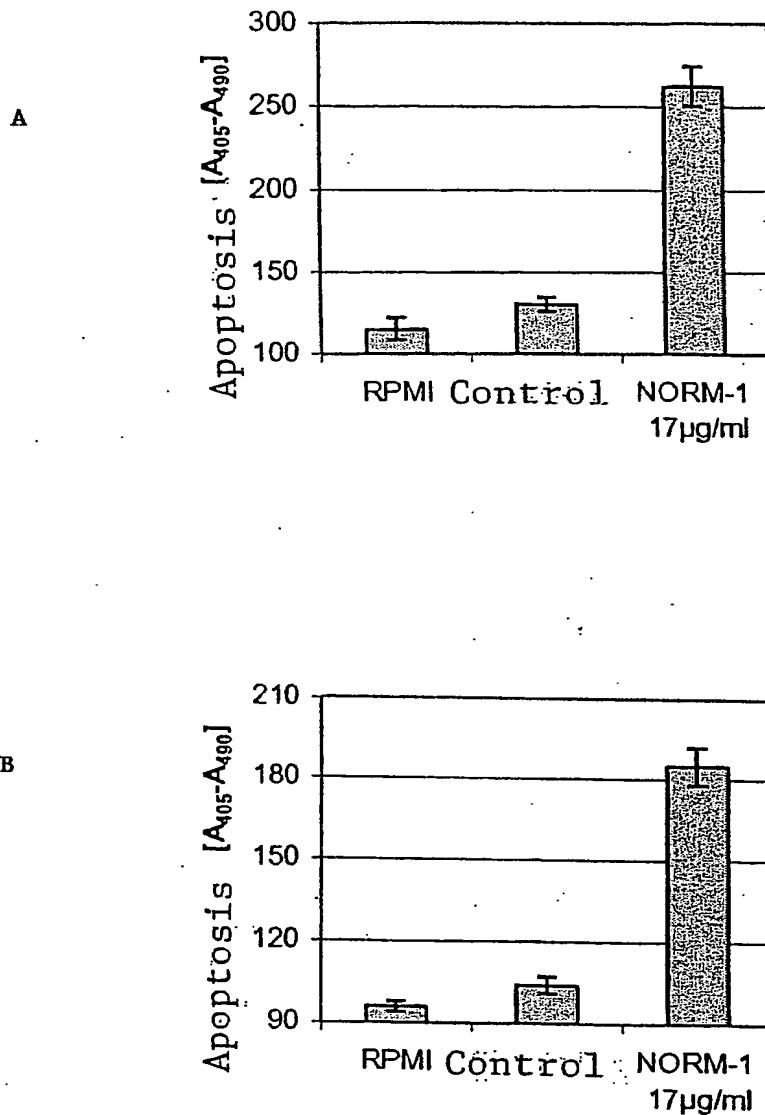


Fig. 5

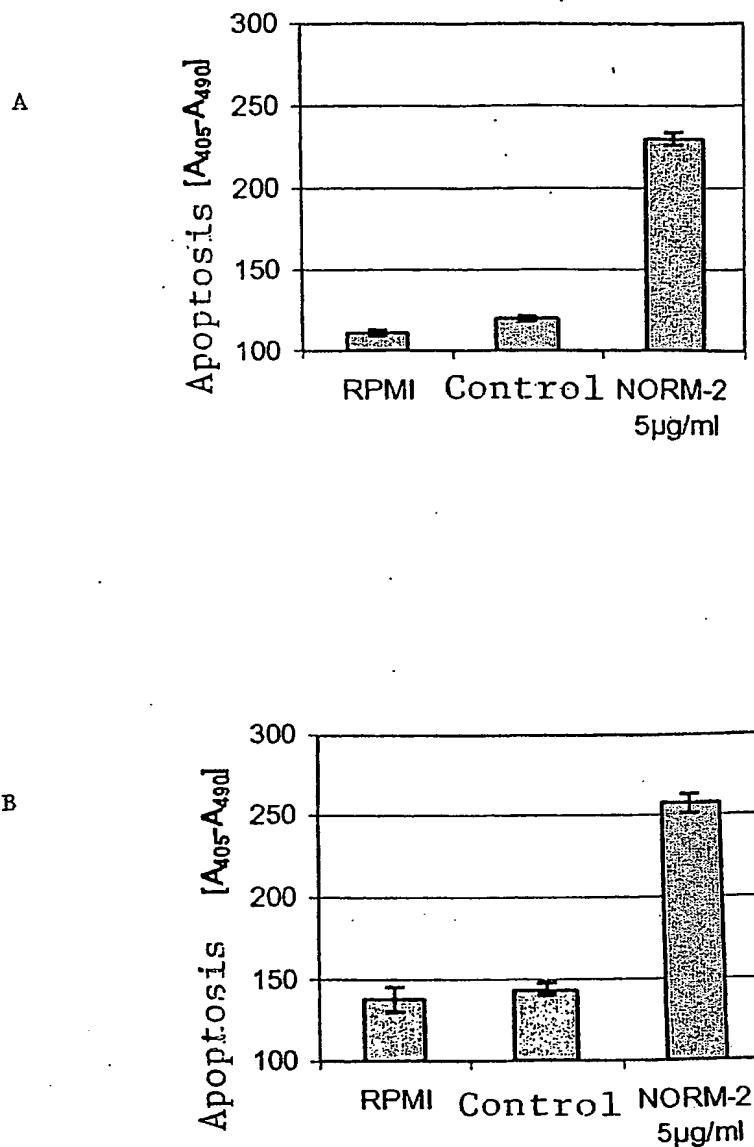


Fig. 6

NORM-1 (VH)

GAG	GTG	CAG	CTG	TTG	GAG	TCT	GGG	GGG	TTG	GTA	CAG	CCT	GGG	GGG	TCC	CTG	AGA	CTC	60	
Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu		
1		5		10		15		20		25		30		35		40		45		
CDR1																				
																			105	
TCC	TGT	GCA	GCC	TCT	GGG	TTC	ACC	TTT	AGC	AGC	TAT	GCC	ATG	AGC	TGG	GTC	CGC	CAG	GCT	120
Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	
																			40	
CDR2																				
																			148	
CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTC	TCA	GCT	ATT	AGT	GGT	GGT	AGC	ACA	TAC	TAC		180	
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Ala	Ile	Ser	Gly	Ser	Gly	Ser	Thr	Tyr	Tyr		
																			60	
CDR3																				
																			198	
GCA	GAC	TCC	GTG	AAG	GCC	CGG	TTC	ACC	ATC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	ACG	CTG	TAT	240
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
																			80	
																			65	
																			70	
																			75	
																			85	
																			90	
																			95	
																			100	
D-Region																				
																			321	
TAT	GAT	AGT	AGT	GGT	TAT	TAT	TAT	TAC	ATG	GAC	GTC	(SEQ. ID. NO: 2) 357								
Tyr	Asp	Ser	Ser	Gly	Tyr	Ser	Glu	Glu	Tyr	Met	Asp	Val	(SEQ. ID. NO: 1)							
																			110	
																			115	

NORM-1 (VL)

TCC TAT GTG CTG ACT CAG CCA CCC TCG GTG TCA GTG TCC CCA GGA CAA ACG GCC AGG ATC
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile
1 5 10 15 20 60

CDR1 67 99 CDR2 145 165 CDR3 262 297
ACC TGC TCT GGA GAT GCA TTG CCA AAA TAT GCT TAT GGT TAC CAG CAG AAG TCA GGC
Thr Cys Ser Gly Asp Ala Leu Pro Lys Tyr Ala Tyr Trp Tyr Gln Gln Lys Ser Gly
25 30 35 40 120

CAG GCC CCT GTG CTG GTC ATC TAT GAG GAC AGC AAA CGA CCC TCC GGG ATC CCT GAG AGA
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
45 50 55 60 180

TTC TCT GGC TCC AGC TCA GGG ACA ATG GCC ACC TTG ACT ATC AGT GGT GGG GCC CAG GTG GAG
Phe Ser Gly Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu
65 70 75 80 240

I-Region

GAT GAA GCT GAC TAC TAC TGT TAC TCA ACA GAC AGC AGT GGT AAT CAT AGC TAT GTG TTC (SEQ. ID. NO: 4) 300
Asp Glu Ala Asp Tyr Tyr Cys Ser Thr Asp Ser Ser Gly Asn His Ser Tyr Val Phe (SEQ. ID. NO: 3) 100
85 90 95 100

NORM-2 (VH)

GAG	GTG	CAG	CTG	GTG	GAG	TCT	GGG	GGG	CTG	GTC	AAG	CCT	GGG	TCC	CTG	AGA	CTC	60	
Glu	Val	Gln	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Arg	Leu	
1		5		10		15			20										
CDR1																			
TCC	TGT	GCA	GCC	TCT	GGG	TTC	ACC	TTC	AGT	AGC	TAT	AGC	ATG	AAC	TGG	GTC	CGC	GCT	120
Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ser	Met	Asn	Trp	Val	Arg	Gln	Ala
25				30				35					35					40	
CDR2																			
CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTC	TCA	TCC	ATT	AGT	AGT	AGT	TAC	ATA	TAC	TAC	180	
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Ser	Ser	Ser	Ser	Ser	Tyr	Ile	Tyr	Tyr		
				45				50					55					60	
CDR3																			
GCA	GAC	TCA	GTG	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAC	GCC	AAG	AAC	TCA	TAT	240
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
				65				70			75			75				80	
J-Region																			
CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCG	GAC	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	CAT	GGG	300
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	His	Gly
				85				90			95		95					100	
324																			
AAC	TAC	TAC	TAC	TAC	ATG	GAC	GTC	(SEQ. ID. NO. 6)											
Asn	Tyr	Tyr	Tyr	Tyr	Met	Asp	Val	(SEQ. ID. NO. 5)											
					105														
324																			

NORM-2 (VL)

CAG TCT GTG TTG ACG CAG CCG CCC TCA GTG TCT GGG GCA GGG CAG GTC ACC ATC
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile
1 5 10 15 20

67 CDR1 108

TCC TGC ACT GGG AGC AGC TCC AAC ATC GGG GCA GGT TAT GAT GTC CAC TGG TAC CAG CAG
Ser Cys Thr Gly Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln
25 30 35 40

154 CDR2 174

CTT CCA GGA ACA GCC CCC AAA CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GTC
Leu Pro Gly Thr Ala Pro Lys Leu Ile Tyr Asn Ser Asn Arg Pro Ser Gly Val
45 50 55 60

240

CCT GAC CGG TTC TCT GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC ACT GGG CTC
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

J-Region

271 CDR3 303

CAG GCT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT GCC TTG
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ser Ser Leu Ser Ala Leu
85 90 95 100

300

303

GTA TTC (SEQ. ID. NO: 8)
Val Phe (SEQ. ID. NO: 7)

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